

# Jerry StÅ¥hlberg

## List of Publications by Year in descending order

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81  
papers

7,160  
citations

61857

43  
h-index

64668

79  
g-index

82  
all docs

82  
docs citations

82  
times ranked

5127  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Glucomannan and beta-glucan degradation by <i>Mytilus edulis</i> Cel45A: Crystal structure and activity comparison with GH45 subfamily A, B and C. <i>Carbohydrate Polymers</i> , 2022, 277, 118771.  | 5.1  | 3         |
| 2  | Machine learning reveals sequence-function relationships in family 7 glycoside hydrolases. <i>Journal of Biological Chemistry</i> , 2021, 297, 100931.  | 1.6  | 13        |
| 3  | Reply to Cosgrove: Non-enzymatic action of expansins. <i>Journal of Biological Chemistry</i> , 2020, 295, 6783.   | 1.6  | 0         |
| 4  | Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020, 77, 927-929.   | 4.5  | 71        |
| 5  | The hydrolysis mechanism of a GH45 cellulase and its potential relation to lytic transglycosylase and expansin function. <i>Journal of Biological Chemistry</i> , 2020, 295, 4477-4487.   | 1.6  | 16        |
| 6  | Antibacterial pyrrolidinyl and piperidinyl substituted 2,4-diacetylphloroglucinols from <i>Pseudomonas protegens</i> UP46. <i>Journal of Antibiotics</i> , 2020, 73, 739-747.   | 1.0  | 3         |
| 7  | The dissociation mechanism of processive cellulases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23061-23067.   | 3.3  | 40        |
| 8  | Advantages of a distant cellulase catalytic base. <i>Journal of Biological Chemistry</i> , 2018, 293, 4680-4687.  | 1.6  | 5         |
| 9  | Enantioselective Binding of Propranolol and Analogues Thereof to Cellobiohydrolase Cel7A. <i>Chemistry - A European Journal</i> , 2018, 24, 17975-17985.  | 1.7  | 5         |
| 10 | Side-by-side biochemical comparison of two lytic polysaccharide monooxygenases from the white-rot fungus <i>Heterobasidion irregulare</i> on their activity against crystalline cellulose and glucomannan. <i>PLoS ONE</i> , 2018, 13, e0203430.                            | 1.1  | 7         |
| 11 | Correlation of structure, function and protein dynamics in GH7 cellobiohydrolases from <i>Trichoderma atroviride</i> , <i>T. reesei</i> and <i>T. harzianum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 5.  | 6.2  | 37        |
| 12 | Development of minimal enzyme cocktails for hydrolysis of sulfite-pulped lignocellulosic biomass. <i>Journal of Biotechnology</i> , 2017, 246, 16-23.   | 1.9  | 59        |
| 13 | Improving the thermal stability of cellobiohydrolase Cel7A from <i>Hypocrea jecorina</i> by directed evolution. <i>Journal of Biological Chemistry</i> , 2017, 292, 17418-17430.  | 1.6  | 52        |
| 14 | Biochemical and Structural Characterizations of Two <i>Dictyostelium</i> Cellobiohydrolases from the Amoebozoa Kingdom Reveal a High Level of Conservation between Distant Phylogenetic Trees of Life. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3395-3409. | 1.4  | 13        |
| 15 | Who's on base? Revealing the catalytic mechanism of inverting family 6 glycoside hydrolases. <i>Chemical Science</i> , 2016, 7, 5955-5968.  | 3.7  | 27        |
| 16 | Sequencing, biochemical characterization, crystal structure and molecular dynamics of cellobiohydrolase Cel7A from <i>Geotrichum candidum</i> 3C. <i>FEBS Journal</i> , 2015, 282, 4515-4537.   | 2.2  | 37        |
| 17 | Structural insights into the inhibition of cellobiohydrolase Cel7A by xylooligosaccharides. <i>FEBS Journal</i> , 2015, 282, 2167-2177.   | 2.2  | 25        |
| 18 | Fungal Cellulases. <i>Chemical Reviews</i> , 2015, 115, 1308-1448.  | 23.0 | 673       |

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|----|---|-----|-----------|
| 19 | Quantum mechanical calculations suggest that lytic polysaccharide monooxygenases use a copper-oxy, oxygen-rebound mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 149-154.                   | 3.3 | 210       |
| 20 | Adaptation of <i>Dekkera bruxellensis</i> to lignocellulose-based substrate. Biotechnology and Applied Biochemistry, 2014, 61, 51-57.   | 1.4 | 17        |
| 21 | Expression, crystal structure and cellulase activity of the thermostable cellobiohydrolase Cel7A from the fungus <i>Hemicola grisea</i> var. <i>thermoidea</i> . Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2356-2366. | 2.5 | 26        |
| 22 | Towards a molecular-level theory of carbohydrate processivity in glycoside hydrolases. Current Opinion in Biotechnology, 2014, 27, 96-106.  | 3.3 | 89        |
| 23 | The Mechanism of Cellulose Hydrolysis by a Two-Step, Retaining Cellobiohydrolase Elucidated by Structural and Transition Path Sampling Studies. Journal of the American Chemical Society, 2014, 136, 321-329.                                       | 6.6 | 164       |
| 24 | Structural and Electronic Snapshots during the Transition from a Cu(II) to Cu(I) Metal Center of a Lytic Polysaccharide Monooxygenase by X-ray Photoreduction. Journal of Biological Chemistry, 2014, 289, 18782-18792.                             | 1.6 | 99        |
| 25 | Carbohydrate-Protein Interactions That Drive Processive Polysaccharide Translocation in Enzymes Revealed from a Computational Study of Cellobiohydrolase Processivity. Journal of the American Chemical Society, 2014, 136, 8810-8819.              | 6.6 | 95        |
| 26 | Crystal Structure and Computational Characterization of the Lytic Polysaccharide Monooxygenase GH61D from the Basidiomycota Fungus <i>Phanerochaete chrysosporium</i> . Journal of Biological Chemistry, 2013, 288, 12828-12839.                    | 1.6 | 158       |
| 27 | The Structure of a Bacterial Cellobiohydrolase: The Catalytic Core of the Thermobifida fusca Family GH6 Cellobiohydrolase Cel6B. Journal of Molecular Biology, 2013, 425, 622-635.  | 2.0 | 34        |
| 28 | Rational design, synthesis, evaluation and enzyme-substrate structures of improved fluorogenic substrates for family 6 glycoside hydrolases. FEBS Journal, 2013, 280, 184-198.  | 2.2 | 14        |
| 29 | Enhanced ethanol production from wheat straw by integrated storage and pre-treatment (ISP). Enzyme and Microbial Technology, 2013, 52, 105-110.   | 1.6 | 26        |
| 30 | Structural, Biochemical, and Computational Characterization of the Glycoside Hydrolase Family 7 Cellobiohydrolase of the Tree-killing Fungus <i>Heterobasidion irregulare</i> . Journal of Biological Chemistry, 2013, 288, 5861-5872.              | 1.6 | 70        |
| 31 | Loop Motions Important to Product Expulsion in the Thermobifida fusca Glycoside Hydrolase Family 6 Cellobiohydrolase from Structural and Computational Studies. Journal of Biological Chemistry, 2013, 288, 33107-33117.                            | 1.6 | 31        |
| 32 | Glycosylated linkers in multimodular lignocellulose-degrading enzymes dynamically bind to cellulose. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14646-14651.                                       | 3.3 | 149       |
| 33 | Product Binding Varies Dramatically between Processive and Nonprocessive Cellulase Enzymes. Journal of Biological Chemistry, 2012, 287, 24807-24813.  | 1.6 | 57        |
| 34 | Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.  | 3.5 | 210       |
| 35 | The Putative Endoglucanase PcGH61D from <i>Phanerochaete chrysosporium</i> Is a Metal-Dependent Oxidative Enzyme that Cleaves Cellulose. PLoS ONE, 2011, 6, e27807.   | 1.1 | 226       |
| 36 | Fermentation of lignocellulosic hydrolysate by the alternative industrial ethanol yeast <i>Dekkera bruxellensis</i> . Letters in Applied Microbiology, 2011, 53, 73-78.   | 1.0 | 34        |

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|----|---|-----|-----------|
| 37 | Improved bio-energy yields via sequential ethanol fermentation and biogas digestion of steam exploded oat straw. <i>Bioresource Technology</i> , 2011, 102, 4449-4455.  | 4.8 | 112       |
| 38 | Hypocrea jecorina CEL6A protein engineering. <i>Biotechnology for Biofuels</i> , 2010, 3, 20.   | 6.2 | 55        |
| 39 | Synthesis of Cyclic Î²-Glucan Using Laminarinase 16A Glycosynthase Mutant from the Basidiomycete <i>Phanerochaete chrysosporium</i> . <i>Journal of the American Chemical Society</i> , 2010, 132, 1724-1730.   | 6.6 | 22        |
| 40 | Airtight storage of moist wheat grain improves bioethanol yields. <i>Biotechnology for Biofuels</i> , 2009, 2, 16.  | 6.2 | 17        |
| 41 | X-ray crystal structures of <i>Phanerochaete chrysosporium</i> Laminarinase 16A in complex with products from lichenin and laminarin hydrolysis. <i>FEBS Journal</i> , 2009, 276, 3858-3869.  | 2.2 | 30        |
| 42 | Three-dimensional Crystal Structure and Enzymic Characterization of Î²-Mannanase Man5A from Blue Mussel <i>Mytilus edulis</i> . <i>Journal of Molecular Biology</i> , 2006, 357, 1500-1510.   | 2.0 | 76        |
| 43 | X-ray crystallographic native sulfur SAD structure determination of laminarinase Lam16A from <i>Phanerochaete chrysosporium</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1422-1429.                                  | 2.5 | 13        |
| 44 | Structures of <i>Phanerochaete chrysosporium</i> Cel7D in complex with product and inhibitors. <i>FEBS Journal</i> , 2005, 272, 1952-1964.  | 2.2 | 44        |
| 45 | Structural and biochemical studies of GH family 12 cellulases: improved thermal stability, and ligand complexes. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 89, 246-291.   | 1.4 | 113       |
| 46 | Crystal Complex Structures Reveal How Substrate is Bound in the $\alpha^4$ to the +2 Binding Sites of <i>Humicola grisea</i> Cel12A. <i>Journal of Molecular Biology</i> , 2004, 342, 1505-1517.  | 2.0 | 32        |
| 47 | Structure-Reactivity Studies of <i>Trichoderma reesei</i> Cellobiohydrolase Cel7A. <i>ACS Symposium Series</i> , 2004, , 207-226.   | 0.5 | 4         |
| 48 | Dextranase from <i>Penicillium minioluteum</i> . <i>Structure</i> , 2003, 11, 1111-1121.  | 1.6 | 80        |
| 49 | The catalytic module of Cel7D from <i>Phanerochaete chrysosporium</i> as a chiral selector: structural studies of its complex with the beta blocker (R)-propranolol. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 637-643. | 2.5 | 11        |
| 50 | Engineering the Exo-loop of <i>Trichoderma reesei</i> Cellobiohydrolase, Cel7A. A comparison with <i>Phanerochaete chrysosporium</i> Cel7D. <i>Journal of Molecular Biology</i> , 2003, 333, 817-829.   | 2.0 | 152       |
| 51 | The Active Site of Cellobiohydrolase Cel6A from <i>Trichoderma reesei</i> : The Roles of Aspartic Acids D221 and D175. <i>Journal of the American Chemical Society</i> , 2002, 124, 10015-10024.  | 6.6 | 133       |
| 52 | Preparation and crystallization of selenomethionyl dextranase from <i>Penicillium minioluteum</i> expressed in <i>Pichia pastoris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 346-348.                              | 2.5 | 23        |
| 53 | Crystallization and X-ray analysis of native and selenomethionyl Î²-mannanase Man5A from blue mussel, <i>Mytilus edulis</i> , expressed in <i>Pichia pastoris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 542-545.  | 2.5 | 10        |
| 54 | Structural basis for enantiomer binding and separation of a common Î²-blocker: crystal structure of cellobiohydrolase Cel7A with bound (S)-propranolol at 1.9 Å... resolution. <i>Journal of Molecular Biology</i> , 2001, 305, 79-93.                        | 2.0 | 61        |

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| 55 | Family 7 cellobiohydrolases from <i>Phanerochaete chrysosporium</i> : crystal structure of the catalytic module of Cel7D (CBH58) at 1.32 Å... resolution and homology models of the isozymes. <i>Journal of Molecular Biology</i> , 2001, 314, 1097-1111. | 2.0 | 101       |
| 56 | The X-ray crystal structure of the <i>Trichoderma reesei</i> family 12 endoglucanase 3, Cel12A, at 1.9 Å... resolution. Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2001, 308, 295-310.   | 2.0 | 121       |
| 57 | Characterization of protein glycoforms with N-linked neutral and phosphorylated oligosaccharides: studies on the glycosylation of endoglucanase 1 (Cel7B) from <i>Trichoderma reesei</i> . <i>Biotechnology and Applied Biochemistry</i> , 2001, 33, 141. | 1.4 | 32        |
| 58 | Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19-30.                    | 1.7 | 59        |
| 59 | Engineering of a glycosidase Family 7 cellobiohydrolase to more alkaline pH optimum: the pH behaviour of <i>Trichoderma reesei</i> Cel7A and its E223S/ A224H/L225V/T226A/D262G mutant. <i>Biochemical Journal</i> , 2001, 356, 19.                       | 1.7 | 29        |
| 60 | Endoglucanase 28 (Cel12A), a new <i>Phanerochaete chrysosporium</i> cellulase. <i>FEBS Journal</i> , 1999, 259, 88-95.  | 0.2 | 75        |
| 61 | Crystallographic evidence for substrate ring distortion and protein conformational changes during catalysis in cellobiohydrolase Cel16A from <i>Trichoderma reesei</i> . <i>Structure</i> , 1999, 7, 1035-1045.   | 1.6 | 164       |
| 62 | High-resolution crystal structures reveal how a cellulose chain is bound in the 50 Å... long tunnel of cellobiohydrolase I from <i>Trichoderma reesei</i> . Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 275, 309-325.                 | 2.0 | 413       |
| 63 | The catalytic amino-acid residues in the active site of cellobiohydrolase 1 are involved in chiral recognition. <i>Journal of Biotechnology</i> , 1997, 57, 115-125.  | 1.9 | 25        |
| 64 | The crystal structure of the catalytic core domain of endoglucanase I from <i>Trichoderma reesei</i> at 3.6 Å... resolution, and a comparison with related enzymes. Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1997, 272, 383-397.         | 2.0 | 238       |
| 65 | Isotherms for adsorption of cellobiohydrolase I and II from <i>Trichoderma reesei</i> on microcrystalline cellulose. <i>Applied Biochemistry and Biotechnology</i> , 1997, 66, 39-56.   | 1.4 | 65        |
| 66 | Cellobiohydrolase I from <i>Trichoderma reesei</i> : Identification of an active-site nucleophile and additional information on sequence including the glycosylation pattern of the core protein. <i>Carbohydrate Research</i> , 1997, 304, 143-154.      | 1.1 | 63        |
| 67 | Effect of potential binding site overlap to binding of cellulose to cellulose: a two-dimensional simulation. <i>FEBS Letters</i> , 1996, 378, 51-56.  | 1.3 | 22        |
| 68 | The active sites of cellulases are involved in chiral recognition: a comparison of cellobiohydrolase 1 and endoglucanase 1. <i>FEBS Letters</i> , 1996, 390, 339-344.   | 1.3 | 54        |
| 69 | Activity Studies and Crystal Structures of Catalytically Deficient Mutants of Cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Molecular Biology</i> , 1996, 264, 337-349.  | 2.0 | 162       |
| 70 | Identification of functionally important amino acids in the cellulose-binding domain of <i>Trichoderma reesei</i> cellobiohydrolase I. <i>Protein Science</i> , 1995, 4, 1056-1064.   | 3.1 | 195       |
| 71 | Cloning and characterization of a cDNA encoding a cellobiose dehydrogenase from the white rot fungus <i>Phanerochaete chrysosporium</i> . <i>FEBS Letters</i> , 1995, 369, 233-238.   | 1.3 | 61        |
| 72 | Adsorption and synergism of cellobiohydrolase I and II of <i>Trichoderma reesei</i> during hydrolysis of microcrystalline cellulose. <i>Biotechnology and Bioengineering</i> , 1994, 44, 1064-1073.   | 1.7 | 97        |

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|----|---|-----|-----------|
| 73 | The three-dimensional crystal structure of the catalytic core of cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Science</i> , 1994, 265, 524-528.  | 6.0 | 605       |
| 74 | A Combined Cellobiose Oxidase/Glucose Oxidase Biosensor for HPLC Determination On-Line of Glucose and Soluble Cellodextrines. <i>Analytical Biochemistry</i> , 1993, 214, 389-396.                                    | 1.1 | 39        |
| 75 | Crystallization and Preliminary X-ray Studies on the Core Proteins of Cellobiohydrolase I and Endoglucanase I from <i>Trichoderma reesei</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 905-907.              | 2.0 | 21        |
| 76 | <i>Trichoderma reesei</i> has no true exo-cellulase: all intact and truncated cellulases produce new reducing end groups on cellulose. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1993, 1157, 107-113. | 1.1 | 137       |
| 77 | Analogs of the cellulose binding domain of cellobiohydrolase I from <i>Trichoderma reesei</i> : Synthesis and binding. , 1993, , 780-781.   |     | 0         |
| 78 | A New Model For Enzymatic Hydrolysis of Cellulose Based on the Two-Domain Structure of Cellobiohydrolase I. <i>Nature Biotechnology</i> , 1991, 9, 286-290.   | 9.4 | 128       |
| 79 | Isolated fungal cellulose terminal domains and a synthetic minimum analogue bind to cellulose. <i>FEBS Letters</i> , 1989, 243, 389-393.  | 1.3 | 76        |
| 80 | A binding-site-deficient, catalytically active, core protein of endoglucanase III from the culture filtrate of <i>Trichoderma reesei</i> . <i>FEBS Journal</i> , 1988, 173, 179-183.                                  | 0.2 | 82        |
| 81 | EGIII, a new endoglucanase from <i>Trichoderma reesei</i> : the characterization of both gene and enzyme. <i>Gene</i> , 1988, 63, 11-21.  | 1.0 | 313       |